

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/567,894A

Source: 1 FWD

Date Processed by STIC: 2/7/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 02/07/2007

PATENT APPLICATION: US/10/567,894A

TIME: 11:41:57

Input Set : N:\efs\02_07_07\10567894a_efs\FBRIC54SeqList.txt

Output Set: N:\CRF4\02072007\J567894A.raw

3 <110> APPLICANT: James, David
 4 Govers, Roland
 6 <120> TITLE OF INVENTION: Novel Translocation Assay
 8 <130> FILE REFERENCE: FBRIC54.001APC
 10 <140> CURRENT APPLICATION NUMBER: US 10/567,894A
 C--> 11 <141> **CURRENT FILING DATE: 2006-02-08**
 13 <150> PRIOR APPLICATION NUMBER: AU2003904237
 14 <151> PRIOR FILING DATE: 2003-08-08
 16 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/001057
 17 <151> PRIOR FILING DATE: 2004-08-09
 19 <160> NUMBER OF SEQ ID NOS: 64
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2128
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (146)..(1672)
 33 <400> SEQUENCE: 1
 34 ggggggtccca tggggccgc cctcgacgt cactccggga ccccgcggc ctccgcaggt 60
 36 tctgcgctcc aggccggagt cagagactcc aggatcggtt ctttcatctt cgccgcccct 120
 38 gcgcgtccag ctcttctaag acgag atg ccg tcg ggc ttc caa cag ata ggc 172
 39 Met Pro Ser Gly Phe Gln Gln Ile Gly
 40 1 5
 42 tcc gaa gat ggg gaa ccc cct cag cag cga gtg act ggg acc ctg gtc 220
 43 Ser Glu Asp Gly Glu Pro Pro Gln Gln Arg Val Thr Gly Thr Leu Val
 44 10 15 20 25
 46 ctt gct gtg ttc tct gcg gtg ctt ggc tcc ctg cag ttt ggg tac aac 268
 47 Leu Ala Val Phe Ser Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn
 48 30 35 40
 50 att ggg gtc atc aat gcc cct cag aag gtg att gaa cag agc tac aat 316
 51 Ile Gly Val Ile Asn Ala Pro Gln Lys Val Ile Glu Gln Ser Tyr Asn
 52 45 50 55
 54 gag acg tgg ctg ggg agg cag ggg cct gag gga ccc agc tcc atc cct 364
 55 Glu Thr Trp Leu Gly Arg Gln Gly Pro Glu Gly Pro Ser Ser Ile Pro
 56 60 65 70
 58 cca ggc acc ctc acc acc ctc tgg gcc ctc tcc gtg gcc atc ttt tcc 412
 59 Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser
 60 75 80 85
 62 gtg ggc ggc atg att tcc tcc ttc ctc att ggt atc atc tct cag tgg 460
 63 Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp
 64 90 95 100 105

see P. 6

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66 ctt gga agg aaa agg gcc atg ctg gtc aac aat gtc ctg gcg gtg ctg      508
67 Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu
68              110              115              120
70 ggg ggc agc ctc atg ggc ctg gcc aac gct gct gcc tcc tat gaa atg      556
71 Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala Ala Ser Tyr Glu Met
72              125              130              135
74 ctc atc ctt gga cga ttc ctc att ggc gcc tac tca ggg ctg aca tca      604
75 Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr Ser Gly Leu Thr Ser
76              140              145              150
78 ggg ctg gtg ccc atg tac gtg ggg gag att gct ccc act cac ctg cgg      652
79 Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala Pro Thr His Leu Arg
80              155              160              165
82 ggc gcc ctg ggg acg ctc aac caa ctg gcc att gtt atc ggc att ctg      700
83 Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile Val Ile Gly Ile Leu
84 170              175              180              185
86 atc gcc cag gtg ctg ggc ttg gag tcc ctc ctg ggc act gcc agc ctg      748
87 Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu Gly Thr Ala Ser Leu
88              190              195              200
90 tgg cca ctg ctc ctg ggc ctc aca gtg cta cct gcc ctc ctg cag ctg      796
91 Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro Ala Leu Leu Gln Leu
92              205              210              215
94 gtc ctg ctg ccc ttc tgt ccc gag agc ccc cgc tac ctc tac atc atc      844
95 Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg Tyr Leu Tyr Ile Ile
96              220              225              230
98 cag aat ctc gag ggg cct gcc aga aag agt ctg aag cgc ctg aca ggc      892
99 Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu Lys Arg Leu Thr Gly
100              235              240              245
102 tgg gcc gat gtt tct gga gtg ctg gct gag ctg aag gat gag aag cgg      940
103 Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu Lys Asp Glu Lys Arg
104 250              255              260              265
106 aag ctg gag cgt gag cgg cca ctg tcc ctg ctc cag ctc ctg ggc agc      988
107 Lys Leu Glu Arg Glu Arg Pro Leu Ser Leu Leu Gln Leu Leu Gly Ser
108              270              275              280
110 cgt acc cac cgg cag ccc ctg atc att gcg gtc gtg ctg cag ctg agc      1036
111 Arg Thr His Arg Gln Pro Leu Ile Ile Ala Val Val Leu Gln Leu Ser
112              285              290              295
114 cag cag ctc tct ggc atc aat gct gtt ttc tat tat tcg acc agc atc      1084
115 Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr Ser Ile
116              300              305              310
118 ttc gag aca gca ggg gta ggc cag cct gcc tat gcc acc ata gga gct      1132
119 Phe Glu Thr Ala Gly Val Gly Gln Pro Ala Tyr Ala Thr Ile Gly Ala
120              315              320              325
122 ggt gtg gtc aac aca gtc ttc acc ttg gtc tcg gtg ttg ttg gtg gag      1180
123 Gly Val Val Asn Thr Val Phe Thr Leu Val Ser Val Leu Leu Val Glu
124 330              335              340              345
126 cgg gcg ggg cgc cgg acg ctc cat ctc ctg ggc ctg gcg ggc atg tgt      1228
127 Arg Ala Gly Arg Arg Thr Leu His Leu Leu Gly Leu Ala Gly Met Cys
128              350              355              360
130 ggc tgt gcc atc ctg atg act gtg gct ctg ctc ctg ctg gag cga gtt      1276

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131 Gly Cys Ala Ile Leu Met Thr Val Ala Leu Leu Leu Leu Glu Arg Val
132          365          370          375
134 cca gcc atg agc tac gtc tcc att gtg gcc atc ttt ggc ttc gtg gca 1324
135 Pro Ala Met Ser Tyr Val Ser Ile Val Ala Ile Phe Gly Phe Val Ala
136          380          385          390
138 ttt ttt gag att ggc cct ggc ccc att cct tgg ttc atc gtg gcc gag 1372
139 Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp Phe Ile Val Ala Glu
140          395          400          405
142 ctc ttc agc cag gga ccc cgc ccg gca gcc atg gct gtg gct ggt ttc 1420
143 Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met Ala Val Ala Gly Phe
144 410          415          420          425
146 tcc aac tgg acg agc aac ttc atc att ggc atg ggt ttc cag tat gtt 1468
147 Ser Asn Trp Thr Ser Asn Phe Ile Ile Gly Met Gly Phe Gln Tyr Val
148          430          435          440
150 gcg gag gct atg ggg ccc tac gtc ttc ctt cta ttt gcg gtc ctc ctg 1516
151 Ala Glu Ala Met Gly Pro Tyr Val Phe Leu Leu Phe Ala Val Leu Leu
152          445          450          455
154 ctg ggc ttc ttc atc ttc acc ttc tta aga gta cct gaa act cga ggc 1564
155 Leu Gly Phe Phe Ile Phe Thr Phe Leu Arg Val Pro Glu Thr Arg Gly
156          460          465          470
158 cgg acg ttt gac cag atc tca gct gcc ttc cac cgg aca ccc tct ctt 1612
159 Arg Thr Phe Asp Gln Ile Ser Ala Ala Phe His Arg Thr Pro Ser Leu
160          475          480          485
162 tta gag cag gag gtg aaa ccc agc aca gaa ctt gag tat tta ggg cca 1660
163 Leu Glu Gln Glu Val Lys Pro Ser Thr Glu Leu Glu Tyr Leu Gly Pro
164 490          495          500          505
166 gat gag aac gac tgaggggccca ggcaggggtg ggagagccag ctctctctac 1712
167 Asp Glu Asn Asp
170 ccggcccca gaccccttcc tttcctctgc agcactttaa ccctctcttc cctattattt 1772
172 ccgggtggaa aagaatccct gcagcctggt agaattggga agctggggga aggggtggtct 1832
174 gagcaccccc tcattccccc cgtgtgactc tcttggatta tttatgtgtt gtggtttggc 1892
176 cgtggccatc aggggtgggcc actctccccc ccctcttccc tcccccatcc cctttcctcc 1952
178 ccaccttccc cagactcagc tccagaatac cttcttcgct gctagagaag ggggattgga 2012
180 gggaagacag gtctagactt tctcagtggg acaaaccaga gcagagagca ggacaggaga 2072
182 caagaaatcc agtttccccc caccttgga cctcccaca atctgggact ttcact 2128
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 509
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2
192 Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
193 1          5          10          15
196 Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
197          20          25          30
200 Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
201          35          40          45
204 Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
205          50          55          60
208 Gly Pro Glu Gly Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu

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209	65					70				75				80		
212	Trp	Ala	Leu	Ser	Val	Ala	Ile	Phe	Ser	Val	Gly	Gly	Met	Ile	Ser	Ser
213					85					90					95	
216	Phe	Leu	Ile	Gly	Ile	Ile	Ser	Gln	Trp	Leu	Gly	Arg	Lys	Arg	Ala	Met
217				100					105					110		
220	Leu	Val	Asn	Asn	Val	Leu	Ala	Val	Leu	Gly	Gly	Ser	Leu	Met	Gly	Leu
221			115					120					125			
224	Ala	Asn	Ala	Ala	Ala	Ser	Tyr	Glu	Met	Leu	Ile	Leu	Gly	Arg	Phe	Leu
225		130					135					140				
228	Ile	Gly	Ala	Tyr	Ser	Gly	Leu	Thr	Ser	Gly	Leu	Val	Pro	Met	Tyr	Val
229	145					150					155				160	
232	Gly	Glu	Ile	Ala	Pro	Thr	His	Leu	Arg	Gly	Ala	Leu	Gly	Thr	Leu	Asn
233				165					170					175		
236	Gln	Leu	Ala	Ile	Val	Ile	Gly	Ile	Leu	Ile	Ala	Gln	Val	Leu	Gly	Leu
237			180						185					190		
240	Glu	Ser	Leu	Leu	Gly	Thr	Ala	Ser	Leu	Trp	Pro	Leu	Leu	Leu	Gly	Leu
241		195						200					205			
244	Thr	Val	Leu	Pro	Ala	Leu	Leu	Gln	Leu	Val	Leu	Leu	Pro	Phe	Cys	Pro
245		210					215					220				
248	Glu	Ser	Pro	Arg	Tyr	Leu	Tyr	Ile	Ile	Gln	Asn	Leu	Glu	Gly	Pro	Ala
249	225					230					235				240	
252	Arg	Lys	Ser	Leu	Lys	Arg	Leu	Thr	Gly	Trp	Ala	Asp	Val	Ser	Gly	Val
253				245					250					255		
256	Leu	Ala	Glu	Leu	Lys	Asp	Glu	Lys	Arg	Lys	Leu	Glu	Arg	Glu	Arg	Pro
257			260					265					270			
260	Leu	Ser	Leu	Leu	Gln	Leu	Leu	Gly	Ser	Arg	Thr	His	Arg	Gln	Pro	Leu
261		275						280					285			
264	Ile	Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser	Gly	Ile	Asn
265		290					295					300				
268	Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Thr	Ala	Gly	Val	Gly
269	305					310					315				320	
272	Gln	Pro	Ala	Tyr	Ala	Thr	Ile	Gly	Ala	Gly	Val	Val	Asn	Thr	Val	Phe
273				325					330					335		
276	Thr	Leu	Val	Ser	Val	Leu	Leu	Val	Glu	Arg	Ala	Gly	Arg	Arg	Thr	Leu
277			340						345				350			
280	His	Leu	Leu	Gly	Leu	Ala	Gly	Met	Cys	Gly	Cys	Ala	Ile	Leu	Met	Thr
281		355						360					365			
284	Val	Ala	Leu	Leu	Leu	Leu	Glu	Arg	Val	Pro	Ala	Met	Ser	Tyr	Val	Ser
285		370					375					380				
288	Ile	Val	Ala	Ile	Phe	Gly	Phe	Val	Ala	Phe	Phe	Glu	Ile	Gly	Pro	Gly
289	385					390					395				400	
292	Pro	Ile	Pro	Trp	Phe	Ile	Val	Ala	Glu	Leu	Phe	Ser	Gln	Gly	Pro	Arg
293				405					410					415		
296	Pro	Ala	Ala	Met	Ala	Val	Ala	Gly	Phe	Ser	Asn	Trp	Thr	Ser	Asn	Phe
297			420						425				430			
300	Ile	Ile	Gly	Met	Gly	Phe	Gln	Tyr	Val	Ala	Glu	Ala	Met	Gly	Pro	Tyr
301		435						440				445				
304	Val	Phe	Leu	Leu	Phe	Ala	Val	Leu	Leu	Leu	Gly	Phe	Phe	Ile	Phe	Thr
305		450					455					460				

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308 Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser
309 465                               470                               475                               480
312 Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro
313                               485                               490                               495
316 Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
317                               500                               505
320 <210> SEQ ID NO: 3
321 <211> LENGTH: 1566
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Homo sapiens GLUT4 with HA tag
329 <220> FEATURE:
330 <221> NAME/KEY: CDS
331 <222> LOCATION: (1)..(1566)
333 <400> SEQUENCE: 3
334 atg ccg tcg ggc ttc caa cag ata ggc tcc gaa gat ggg gaa ccc cct      48
335 Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
336 1                               5                               10                               15
338 cag cag cga gtg act ggg acc ctg gtc ctt gct gtg ttc tct gcg gtg      96
339 Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
340                               20                               25                               30
342 ctt ggc tcc ctg cag ttt ggg tac aac att ggg gtc atc aat gcc cct      144
343 Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
344                               35                               40                               45
346 cag aag gtg att gaa cag agc tac aat gag acg tgg ctg ggg agg cag      192
347 Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
348                               50                               55                               60
350 ggg cct gag atc gat tat cct tat gat gtt cct gat tat gct gag gga      240
351 Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly
352 65                               70                               75                               80
354 ccc agc tcc atc cct cca ggc acc ctc acc acc ctc tgg gcc ctc tcc      288
355 Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser
356                               85                               90                               95
358 gtg gcc atc ttt tcc gtg ggc ggc atg att tcc tcc ttc ctc att ggt      336
359 Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly
360                               100                              105                              110
362 atc atc tct cag tgg ctt gga agg aaa agg gcc atg ctg gtc aac aat      384
363 Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn
364                               115                              120                              125
366 gtc ctg gcg gtg ctg ggg ggc agc ctc atg ggc ctg gcc aac gct gct      432
367 Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala
368                               130                              135                              140
370 gcc tcc tat gaa atg ctc atc ctt gga cga ttc ctc att ggc gcc tac      480
371 Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr
372 145                               150                               155                               160
374 tca ggg ctg aca tca ggg ctg gtg ccc atg tac gtg ggg gag att gct      528
375 Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala
376                               165                               170                               175

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/567,894A

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Input Set : N:\efs\02_07_07\10567894a_efs\FBRIC54SeqList.txt
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FyL

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:57; Xaa Pos. 227,436

Seq#:58; Xaa Pos. 227,436

VERIFICATION SUMMARY

DATE: 02/07/2007

PATENT APPLICATION: US/10/567,894A

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Input Set : N:\efs\02_07_07\10567894a_efs\FBRIC54SeqList.txt

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:7336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:789

M:341 Repeated in SeqNo=57

L:7562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:224

M:341 Repeated in SeqNo=58